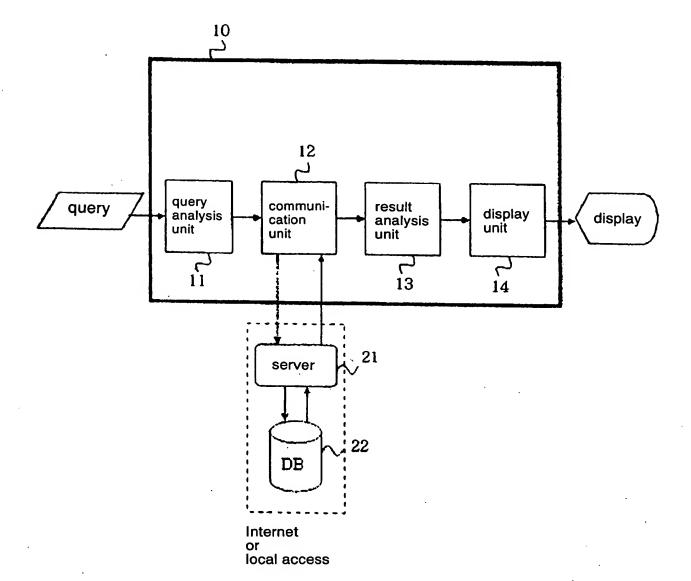Tomoya MIYAKAWA et al.
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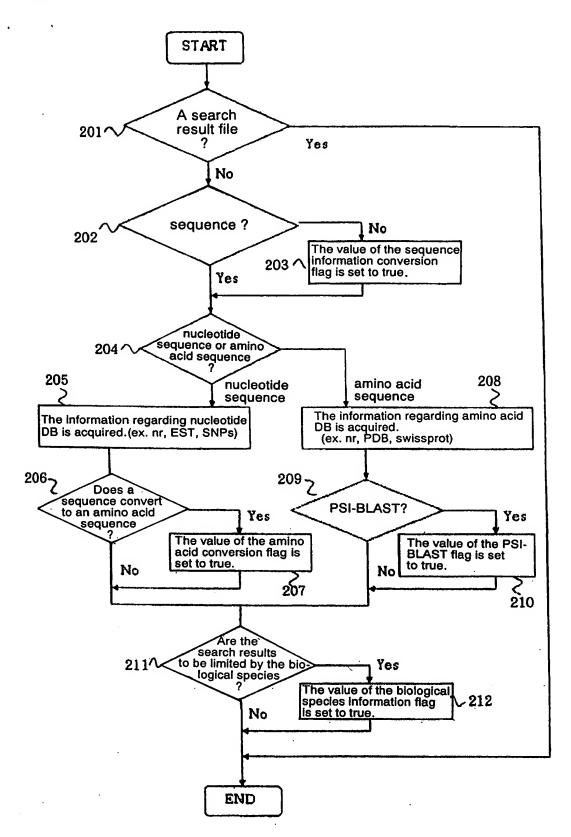Q78853-------Filed December 8, 2003---Sheets __1__ of 13

◦Fig. 1

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Fig. 2

START

201 — A search result file ?

Yes

No

202 — sequence ?

No

203 — The value of the sequence information conversion flag is set to true.

Yes

204 — nucleotide sequence or amino acid sequence ?

nucleotide sequence

amino acid sequence

205 — The information regarding nucleotide DB is acquired.(ex. nr, EST, SNPs)

208 — The information regarding amino acid DB is acquired. (ex. nr, PDB, swissprot)

206 — Does a sequence convert to an amino acid sequence ?

Yes

The value of the amino acid conversion flag is set to true.

207

No

209 — PSI-BLAST?

Yes

The value of the PSI-BLAST flag is set to true.

No

210

211 — Are the search results to be limited by the biological species ?

Yes

The value of the biological species information flag is set to true. — 212

No

END

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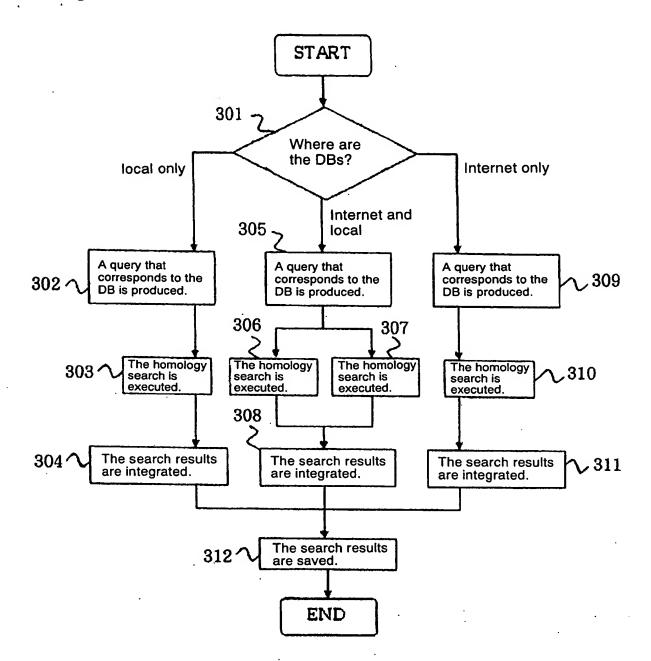## Fig. 3

START

301 — Where are the DBs?

local only

Internet and local

Internet only

305 —

302 — A query that corresponds to the DB is produced.

A query that corresponds to the DB is produced.

A query that corresponds to the DB is produced. — 309

306

307

303 — The homology search is executed.

The homology search is executed.

The homology search is executed.

The homology search is executed. — 310

308

304 — The search results are integrated.

The search results are integrated.

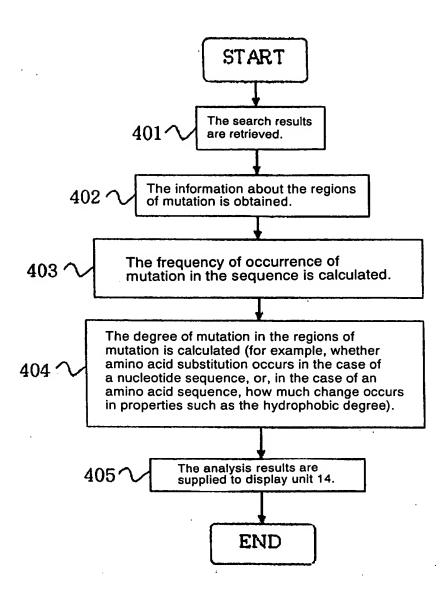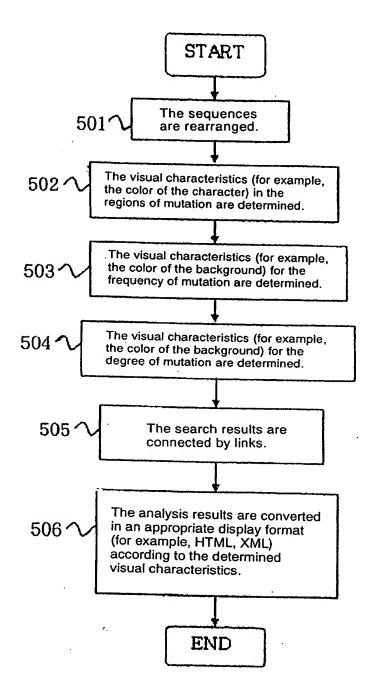The search results are integrated. — 311

312 — The search results are saved.

END

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Fig. 4

START

401 — The search results are retrieved.

402 — The information about the regions of mutation is obtained.

403 — The frequency of occurrence of mutation in the sequence is calculated.

404 — The degree of mutation in the regions of mutation is calculated (for example, whether amino acid substitution occurs in the case of a nucleotide sequence, or, in the case of an amino acid sequence, how much change occurs in properties such as the hydrophobic degree).

405 — The analysis results are supplied to display unit 14.

END

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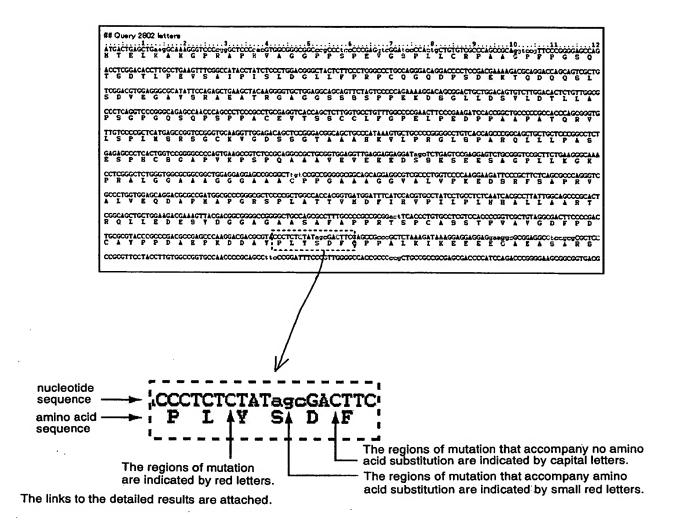Q78853-------Filed December 8, 2003---Sheets _5_ of 13

Fig. 5

START

501 — The sequences are rearranged.

502 — The visual characteristics (for example, the color of the character) in the regions of mutation are determined.

503 — The visual characteristics (for example, the color of the background) for the frequency of mutation are determined.

504 — The visual characteristics (for example, the color of the background) for the degree of mutation are determined.

505 — The search results are connected by links.

506 — The analysis results are converted in an appropriate display format (for example, HTML, XML) according to the determined visual characteristics.

END

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. Fig.· 6

Blast Auto Submition Form

If you submit, your query send to NCBI BLAST, and parse results.

Enter your Query

or Enter Query File [   ] [Ref...]

Choose database ☑Human nr ☑Human EST ☑Human SNPs
Limit by entrez query select from: [Homo sapiens [ORGN]   ]

Display translated codon ☑check this out. ex.)query is promoter

To submit the query. [Submit] To clear the form [Clear]

Blast Result Parser Form

If you submit, parse BLAST Result.

Enter your Query

or Enter Query File [   ] [Ref...]

Enter Blast Result File [   ] [Ref...]
Enter Blast Result File [   ] [Ref...]
Enter Blast Result File [   ] [Ref...]

To submit the query. [Submit] To clear the form [Clear]

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· Fig: 7

nucleotide sequence

amino acid sequence

The regions of mutation are indicated by red letters.

The regions of mutation that accompany no amino acid substitution are indicated by capital letters.

The regions of mutation that accompany amino acid substitution are indicated by small red letters.

The links to the detailed results are attached.

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·Fig. 8

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Fig. 9

Blast Auto Submition Form

If you submit, your query send to NCBI BLAST, and parse results.

Enter your Query

or Enter Query File [＿＿＿＿＿] [Ref....]

Choose database [nr ▾]
Limit by entrez query select from: [(none) ▾]
PSI BLAST iteration [1] 1 means standard blastp

To submit the query. [Submit] To clear the form [Clear]

Blast Result Parser Form

If you submit, parse BLAST Result.

Enter your Query

or Enter Query File [＿＿＿＿＿] [Ref....]

Enter Blast Result File [＿＿＿＿＿] [Ref....]
Enter Blast Result File [＿＿＿＿＿] [Ref....]
Enter Blast Result File [＿＿＿＿＿] [Ref....]

To submit the query. [Submit] To clear the form [Clear]

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Fig. 10

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Fig. 11

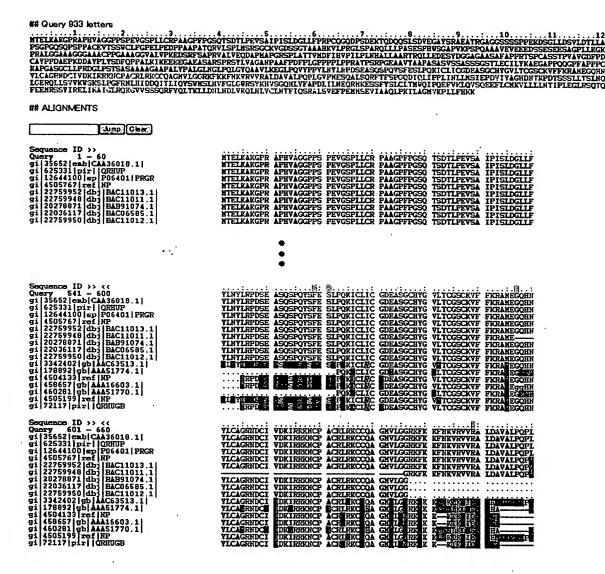|	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	B	Z	X	*
A	4	-1	-2	-2	0	-1	-1	0	-2	-1	-1	-1	-1	-2	-1	1	0	-3	-2	0	-2	-1	0	-4
R	-1	5	0	-2	-3	1	0	-2	0	-3	-2	2	-1	-3	-2	-1	-1	-3	-2	-3	-1	0	-1	-4
N	-2	0	6	1	-3	0	0	0	1	-3	-3	0	-2	-3	-2	1	0	-4	-2	-3	3	0	-1	-4
D	-2	-2	1	6	-3	0	2	-1	-1	-3	-4	-1	-3	-3	-1	0	-1	-4	-3	-3	4	1	-1	-4
C	0	-3	-3	-3	9	-3	-4	-3	-3	-1	-1	-3	-1	-2	-3	-1	-1	-2	-2	-1	-3	-3	-2	-4
Q	-1	1	0	0	-3	5	2	-2	0	-3	-2	1	0	-3	-1	0	-1	-2	-1	-2	0	3	-1	-4
E	-1	0	0	2	-4	2	5	-2	0	-3	-3	1	-2	-3	-1	0	-1	-3	-2	-2	1	4	-1	-4
G	0	-2	0	-1	-3	-2	-2	6	-2	-4	-4	-2	-3	-3	-2	0	-2	-2	-3	-3	-1	-2	-1	-4
H	-2	0	1	-1	-3	0	0	-2	8	-3	-3	-1	-2	-1	-2	-1	-2	-2	2	-3	0	0	-1	-4
I	-1	-3	-3	-3	-1	-3	-3	-4	-3	4	2	-3	1	0	-3	-2	-1	-3	-1	3	-3	-3	-1	-4
L	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	4	-2	2	0	-3	-2	-1	-2	-1	1	-4	-3	-1	-4
K	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	5	-1	-3	-1	0	-1	-3	-2	-2	0	1	-1	-4
M	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2	-1	5	0	-2	-1	-1	-1	-1	1	-3	-1	-1	-4
F	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	6	-4	-2	-2	1	3	-1	-3	-3	-1	-4
P	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	7	-1	-1	-4	-3	-2	-2	-1	-2	-4
S	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	4	1	-3	-2	-2	0	0	0	-4
T	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5	-2	-2	0	-1	-1	0	-4
W	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	11	2	-3	-4	-3	-2	-4
Y	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7	-1	-3	-2	-1	-4
V	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	4	-3	-2	-1	-4
B	-2	-1	3	4	-3	0	1	-1	0	-3	-4	0	-3	-3	-2	0	-1	-4	-3	-3	4	1	-1	-4
Z	-1	0	0	1	-3	3	4	-2	0	-3	-3	1	-1	-3	-1	0	-1	-3	-2	-2	1	4	-1	-4
X	0	-1	-1	-1	-2	-1	-1	-1	-1	-1	-1	-1	-1	-2	-2	0	0	-2	-1	-1	-1	-1	-1	-4
*	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	1

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Fig. 12

>gi|20810385|gb|BC028856.1| LU Mus musculus, solute carrier family 26, member 6, clone MGC:25824
IMAGE:4165725, mRNA, complete cds
Length = 2681

Score = 44.1 bits (22), Expect = 1.1
Identities = 85/106 (80%)
Strand = Plus / Plus

```
Query: 1282 cacagtaaccaggagctcgtgcctctcggtctcagtaacacagtggaggcttcttccag 1341
            |||||||||||||||||| || || || || ||||||||   | ||||| |||||||||
Sbjct: 1220 gacagtaaccaggagctggtagcccttggcctcagtaacctcattggaggcttcttccag 1279
```

```
Query: 1342 tgctactgcgtcacctcctccatgtcccgtagcctggtgcaggaga 1387
            |||| | ||| | || ||||||||| || ||| |||| |||||||
Sbjct: 1280 tgcttccccgtgagctgctccatgtctcggagcttggtacaggaga 1325
```

Score = 44.1 bits (22), Expect = 1.1
Identities = 25/26 (96%)
Strand = Plus / Plus

```
Query: 1805 tgtactttgccaatgctgagctctac 1830
            ||||||| ||||||||||||||||||
Sbjct: 1743 tgtacttcgccaatgctgagctctac 1768
```

>gi|22775306|gb|AY049076.1| LU Mus musculus anion exchanger SLC26A6a mRNA, complete cds
Length = 2552

Score = 44.1 bits (22), Expect = 1.1
Identities = 85/106 (80%)
Strand = Plus / Plus

```
Query: 1282 cacagtaaccaggagctcgtgcctctcggtctcagtaacacagtggaggcttcttccag 1341
            |||||||||||||||||| || || || || ||||||||   | ||||| |||||||||
Sbjct: 1156 gacagtaaccaggagctggtagcccttggcctcagtaacctcattggaggcttcttccag 1215
```

```
Query: 1342 tgctactgcgtcacctcctccatgtcccgtagcctggtgcaggaga 1387
            |||| | ||| | || ||||||||| || ||| |||| |||||||
Sbjct: 1216 tgcttccccgtgagctgctccatgtctcggagcttggtacaggaga 1261
```

Score = 44.1 bits (22), Expect = 1.1
Identities = 25/26 (96%)
Strand = Plus / Plus

```
Query: 1805 tgtactttgccaatgctgagctctac 1830
            ||||||| ||||||||||||||||||
Sbjct: 1679 tgtacttcgccaatgctgagctctac 1704
```

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Fig. 13